

Environmental Science

ANAYLYSIS OF HEAVY METAL REGULATED GENES IN *SINORHIZOBIUM MELILOTI*

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Heavy metals such as zinc, copper and nickel frequently exist in the environment, especially in the soil, in cationic form. These metals are essential for microorganisms in trace amounts but can be toxic at high concentrations. To prevent harming themselves, these microorganisms have evolved homeostatic mechanisms to maintain a safe amount of essential heavy metal cations in their cells. Efforts to understand such homeostatic mechanisms can lead to the development of biomarkers for heavy metals in the environment. This study analyzes the effects of heavy metals on the symbiotic, nitrogen-fixing bacterium *Sinorhizobium meliloti*, with the aim to discover genes that are regulated by heavy metal cations. A bank of *S. meliloti* mutants was created using a mini-transposon of Tn5 carrying the green fluorescent protein (GFP) reporter gene. These mutants were screened for differential GFP gene expression in the presence of zinc and copper ions, using ultraviolet (UV) light. A few mutants were found to show significant increase in gene expression and the DNA regions adjacent to the transposon are currently being analyzed. Several mutants from this mutant bank were also used to measure their growth characteristics in the presence of other metals. Interestingly, one mutant was found to be significantly sensitive to nickel, indicating that the GFP reporter gene had inserted into a gene that could play an important role in nickel homeostasis. Furthermore, this particular mutant is also sensitive to zinc, copper and cadmium ions although to a lesser extent. Genetic analysis of the flanking genes will provide better understanding of bacterial metal homeostasis in *S. meliloti*. It would also be very useful for future phytoremediation efforts as *S. meliloti* is commonly found to be the symbiont of alfalfa, the planting of which can be used to improve soil conditions.